SEQUENCE LISTING

<110> WATANABE, Eijiro
OEDA, Kenji

<120> Raffinose Synthase Genes and Their Use

<130> 0020-4348P

<140> 08/992,914
<141> 1997-12-18

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<170> PatentIn Ver. 2.0

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ata acc aaa act gca acc ctc caa gac gta ata agc acc atc gat att   163
Ile Thr Lys Thr Ala Thr Leu Gln Asp Val Ile Ser Thr Ile Asp Ile
                10                  15                  20

ggt aat ggt aac tca ccc tta ttc tcc ata acc tta gac caa tca cgt   211
Gly Asn Gly Asn Ser Pro Leu Phe Ser Ile Thr Leu Asp Gln Ser Arg
            25                  30                  35

gac ttc ctt gca aat ggc cac cct ttc ctc acc caa gtc cca cct aac   259
Asp Phe Leu Ala Asn Gly His Pro Phe Leu Thr Gln Val Pro Pro Asn
        40                  45                  50

ata aca aca aca aca aca acc act gct tcc tct ttt ctc aat ctc aaa   307
Ile Thr Thr Thr Thr Thr Thr Thr Ala Ser Ser Phe Leu Asn Leu Lys
    55                  60                  65

tcc aac aaa gat acc att ccc aac aac aac aac acc atg ttg ttg caa   355
Ser Asn Lys Asp Thr Ile Pro Asn Asn Asn Asn Thr Met Leu Leu Gln
70                  75                  80                  85

caa ggt tgt ttc gtt ggt ttc aac tcc acc gaa ccc aaa agc cac cac   403
Gln Gly Cys Phe Val Gly Phe Asn Ser Thr Glu Pro Lys Ser His His
                90                  95                  100

gta gtt cca ctc ggc aaa cta aaa gga atc aaa ttc atg agc ata ttc   451
Val Val Pro Leu Gly Lys Leu Lys Gly Ile Lys Phe Met Ser Ile Phe
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cgg ttc aaa gtt tgg tgg aca act cac tgg gtc gga aca aat gga cag   499
Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Thr Asn Gly Gln
        120                 125                 130

gaa cta caa cac gaa aca caa atg tta atc ctg gac aaa aac gac tcc   547
Glu Leu Gln His Glu Thr Gln Met Leu Ile Leu Asp Lys Asn Asp Ser
    135                 140                 145

ctc gga cga ccc tat gtc tta ctc ctc cca atc cta gaa aac acc ttc   595
Leu Gly Arg Pro Tyr Val Leu Leu Leu Pro Ile Leu Glu Asn Thr Phe
150                 155                 160                 165

cga acc tca ctc caa ccc ggt ctc aac gat cac ata ggc atg tcc gtc   643
Arg Thr Ser Leu Gln Pro Gly Leu Asn Asp His Ile Gly Met Ser Val
                170                 175                 180

gaa agc ggt tca aca cat gtc acc ggg tca agc ttc aaa gca tgt ctt   691
Glu Ser Gly Ser Thr His Val Thr Gly Ser Ser Phe Lys Ala Cys Leu
            185                 190                 195

tac atc cat ctc agt aac gac cca tac agt ata cta aaa gaa gca gtt   739
Tyr Ile His Leu Ser Asn Asp Pro Tyr Ser Ile Leu Lys Glu Ala Val
        200                 205                 210

aaa gta atc caa act cag tta gga aca ttc aag act ctt gaa gaa aaa   787
Lys Val Ile Gln Thr Gln Leu Gly Thr Phe Lys Thr Leu Glu Glu Lys
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aca gca cct agt att ata gac aaa ttc ggt tgg tgc acg tgg gat gct   835
Thr Ala Pro Ser Ile Ile Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala
230                 235                 240                 245

ttt tac ttg aag gtt cat cca aaa ggt gta tgg gaa ggt gta aag tct   883
Phe Tyr Leu Lys Val His Pro Lys Gly Val Trp Glu Gly Val Lys Ser
                250                 255                 260

ctc aca gat ggt ggt tgt cct ccc ggt ttc gtc ata atc gac gac ggt   931
Leu Thr Asp Gly Gly Cys Pro Pro Gly Phe Val Ile Ile Asp Asp Gly
            265                 270                 275

tgg caa tcc att tgt cat gac gat gac gat gaa gat gat tca gga atg   979
Trp Gln Ser Ile Cys His Asp Asp Asp Asp Glu Asp Asp Ser Gly Met
        280                 285                 290

aac cga acc tca gcc ggg gaa caa atg cca tgc aga ctt gta aaa tac   1027
Asn Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Val Lys Tyr
    295                 300                 305

gaa gag aat tct aag ttt aga gaa tat gag aat cct gaa aat gga ggg   1075
Glu Glu Asn Ser Lys Phe Arg Glu Tyr Glu Asn Pro Glu Asn Gly Gly
310                 315                 320                 325

aag aaa ggt ttg ggt ggt ttt gtg agg gat ttg aag gaa gag ttt ggg   1123
Lys Lys Gly Leu Gly Gly Phe Val Arg Asp Leu Lys Glu Glu Phe Gly
                330                 335                 340

agt gtg gag agt gtt tat gtt tgg cat gcg ctt tgt ggg tat tgg ggc   1171
Ser Val Glu Ser Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly
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ggg gtt agg cct gga gtg cat ggg atg ccg aaa gct agg gtt gtt gtt   1219
Gly Val Arg Pro Gly Val His Gly Met Pro Lys Ala Arg Val Val Val
        360                 365                 370

ccg aag gtg tct cag ggg ttg aag atg acg atg gag gat ttg gcg gtg   1267
Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met Glu Asp Leu Ala Val
    375                 380                 385

gat aag att gtt gag aac ggt gtg ggg cta gtg ccg cca gat ttt gca   1315
Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val Pro Pro Asp Phe Ala
390                 395                 400                 405

cat gag atg ttt gat ggg ctt cac tct cat ttg gag tcg gcg gga att   1363
His Glu Met Phe Asp Gly Leu His Ser His Leu Glu Ser Ala Gly Ile
                410                 415                 420

gac ggt gtt aaa gtt gat gtt atc cat ctg ctt gag tta cta tca gag   1411
Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Leu Leu Ser Glu
            425                 430                 435

gaa tat ggt gga cga gtt gag cta gca aga gct tat tac aaa gca cta   1459
Glu Tyr Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu
        440                 445                 450

acc tca tca gtg aag aaa cat ttc aaa ggc aat ggt gta att gct agc   1507
Thr Ser Ser Val Lys Lys His Phe Lys Gly Asn Gly Val Ile Ala Ser
    455                 460                 465

atg gag cat tgc aac gac ttc ttt ctc ctc ggc acc gaa gcc ata tcc   1555
Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu Ala Ile Ser
470                 475                 480                 485

ctc ggc cgc gtc gga gat gat ttt tgg tgc tct gat cca tct ggt gat   1603
Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser Asp Pro Ser Gly Asp
                490                 495                 500

cca aat ggt aca tat tgg ctc caa ggt tgt cac atg gta cat tgt gcc   1651
Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys Ala
            505                 510                 515

tac aac agt tta tgg atg gga aat ttc att cag cca gat tgg gac atg   1699
Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp Trp Asp Met
        520                 525                 530

ttt cag tcc act cat cct tgt gct gaa ttt cat gcc gcc tca cga gcc   1747
Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala Ser Arg Ala
    535                 540                 545

ata tcc ggc gga cca att tat gtt agt gat tgt gtt ggt aat cac aat   1795
Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Cys Val Gly Asn His Asn
550                 555                 560                 565

ttc aag ttg ctc aaa tct ctt gtt ttg ccc gat ggt tct atc ttg cgt   1843
Phe Lys Leu Leu Lys Ser Leu Val Leu Pro Asp Gly Ser Ile Leu Arg
                570                 575                 580

tgt caa cat tac gca ctc cct aca aga gat tgc ttg ttt gaa gac cct   1891
Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp Pro
            585                 590                 595
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ttg cat aat ggc aaa aca atg ctg aaa att tgg aat ctc aac aaa tat   1939
Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys Tyr
        600                 605                 610

aca ggt gtt ttg ggt ctt ttc aac tgc caa ggt ggt ggg tgg tgt cct   1987
Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp Cys Pro
    615                 620                 625

gag gca cgg cga aac aag agt gta tct gaa ttt tca cgc gcg gtg aca   2035
Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe Ser Arg Ala Val Thr
630                 635                 640                 645

tgt tat gca agt ccc gaa gac att gaa tgg tgc aat ggg aaa act cca   2083
Cys Tyr Ala Ser Pro Glu Asp Ile Glu Trp Cys Asn Gly Lys Thr Pro
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atg agc acc aaa ggt gtg gat ttt ttt gct gtg tat ttt ttc aag gag   2131
Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val Tyr Phe Phe Lys Glu
            665                 670                 675

aag aaa ttg agg ctc atg aag tgt tct gat aga ttg aaa gtt tcg ctt   2179
Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg Leu Lys Val Ser Leu
        680                 685                 690

gag cca ttt agt ttt gag cta atg aca gtg tct cca gtg aaa gtg ttt   2227
Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser Pro Val Lys Val Phe
    695                 700                 705

tcg aaa agg ttt ata cag ttt gca ccg att ggg tta gtg aac atg ctg   2275
Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu
710                 715                 720                 725

aac tct ggt ggt gcg att cag tct ctg gag ttt gat gat aat gca agt   2323
Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe Asp Asp Asn Ala Ser
                730                 735                 740

ttg gtc aag att ggg gtg aga ggt tgc ggg gag atg agc gtg ttt gcg   2371
Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Ser Val Phe Ala
            745                 750                 755

tct gag aaa ccg gtt tgc tgc aaa att gat ggg gtt aag gtg aaa ttt   2419
Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly Val Lys Val Lys Phe
        760                 765                 770

ctt tat gag gac aaa atg gca aga gtt caa att ctg tgg cct agt tct   2467
Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile Leu Trp Pro Ser Ser
    775                 780                 785

tca aca ttg tct ttg gtc cag ttt tta ttt tgatccctag gaatcctatg     2517
Ser Thr Leu Ser Leu Val Gln Phe Leu Phe
790                 795

cacgtgtctc tgtttacaag tactttatat aagtataata tgtatctatt tccatttta 2577

actgtcttta tgcaattagg tggtcaatta gttatttgtt tgtgaagtaa ctaacttgct 2637

tgtgttgtaa gcttataata tatggtcaag ttcctcactt gtatatacct gttgtatgta 2697

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             20                  25                  30

Leu Asp Gln Ser Arg Asp Phe Leu Ala Asn Gly His Pro Phe Leu Thr
         35                  40                  45

Gln Val Pro Pro Asn Ile Thr Thr Thr Thr Thr Thr Thr Ala Ser Ser
     50                  55                  60

Phe Leu Asn Leu Lys Ser Asn Lys Asp Thr Ile Pro Asn Asn Asn Asn
 65                  70                  75                  80

Thr Met Leu Leu Gln Gln Gly Cys Phe Val Gly Phe Asn Ser Thr Glu
                 85                  90                  95

Pro Lys Ser His His Val Val Pro Leu Gly Lys Leu Lys Gly Ile Lys
            100                 105                 110

Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val
        115                 120                 125

Gly Thr Asn Gly Gln Glu Leu Gln His Glu Thr Gln Met Leu Ile Leu
    130                 135                 140

Asp Lys Asn Asp Ser Leu Gly Arg Pro Tyr Val Leu Leu Leu Pro Ile
145                 150                 155                 160

Leu Glu Asn Thr Phe Arg Thr Ser Leu Gln Pro Gly Leu Asn Asp His
                165                 170                 175

Ile Gly Met Ser Val Glu Ser Gly Ser Thr His Val Thr Gly Ser Ser
            180                 185                 190

Phe Lys Ala Cys Leu Tyr Ile His Leu Ser Asn Asp Pro Tyr Ser Ile
        195                 200                 205

Leu Lys Glu Ala Val Lys Val Ile Gln Thr Gln Leu Gly Thr Phe Lys
    210                 215                 220

Thr Leu Glu Glu Lys Thr Ala Pro Ser Ile Ile Asp Lys Phe Gly Trp
225                 230                 235                 240

Cys Thr Trp Asp Ala Phe Tyr Leu Lys Val His Pro Lys Gly Val Trp
                245                 250                 255

Glu Gly Val Lys Ser Leu Thr Asp Gly Gly Cys Pro Pro Gly Phe Val
            260                 265                 270

Ile Ile Asp Asp Gly Trp Gln Ser Ile Cys His Asp Asp Asp Asp Glu
        275                 280                 285

Asp Asp Ser Gly Met Asn Arg Thr Ser Ala Gly Glu Gln Met Pro Cys
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    290                 295                 300

Arg Leu Val Lys Tyr Glu Glu Asn Ser Lys Phe Arg Glu Tyr Glu Asn
305                 310                 315                 320

Pro Glu Asn Gly Gly Lys Lys Gly Leu Gly Gly Phe Val Arg Asp Leu
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Lys Glu Glu Phe Gly Ser Val Glu Ser Val Tyr Val Trp His Ala Leu
            340                 345                 350

Cys Gly Tyr Trp Gly Gly Val Arg Pro Gly Val His Gly Met Pro Lys
        355                 360                 365

Ala Arg Val Val Val Pro Lys Val Ser Gln Gly Leu Lys Met Thr Met
    370                 375                 380

Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly Leu Val
385                 390                 395                 400

Pro Pro Asp Phe Ala His Glu Met Phe Asp Gly Leu His Ser His Leu
                405                 410                 415

Glu Ser Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu
            420                 425                 430

Glu Leu Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Arg Ala
        435                 440                 445

Tyr Tyr Lys Ala Leu Thr Ser Ser Val Lys Lys His Phe Lys Gly Asn
    450                 455                 460

Gly Val Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly
465                 470                 475                 480

Thr Glu Ala Ile Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Ser
                485                 490                 495

Asp Pro Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His
            500                 505                 510

Met Val His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln
        515                 520                 525

Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His
    530                 535                 540

Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Cys
545                 550                 555                 560

Val Gly Asn His Asn Phe Lys Leu Leu Lys Ser Leu Val Leu Pro Asp
                565                 570                 575

Gly Ser Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys
            580                 585                 590

Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp
        595                 600                 605

Asn Leu Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly
    610                 615                 620
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Gly Gly Trp Cys Pro Glu Ala Arg Arg Asn Lys Ser Val Ser Glu Phe
625                 630                 635                 640

Ser Arg Ala Val Thr Cys Tyr Ala Ser Pro Glu Asp Ile Glu Trp Cys
                645                 650                 655

Asn Gly Lys Thr Pro Met Ser Thr Lys Gly Val Asp Phe Phe Ala Val
            660                 665                 670

Tyr Phe Phe Lys Glu Lys Lys Leu Arg Leu Met Lys Cys Ser Asp Arg
        675                 680                 685

Leu Lys Val Ser Leu Glu Pro Phe Ser Phe Glu Leu Met Thr Val Ser
    690                 695                 700

Pro Val Lys Val Phe Ser Lys Arg Phe Ile Gln Phe Ala Pro Ile Gly
705                 710                 715                 720

Leu Val Asn Met Leu Asn Ser Gly Gly Ala Ile Gln Ser Leu Glu Phe
                725                 730                 735

Asp Asp Asn Ala Ser Leu Val Lys Ile Gly Val Arg Gly Cys Gly Glu
            740                 745                 750

Met Ser Val Phe Ala Ser Glu Lys Pro Val Cys Cys Lys Ile Asp Gly
        755                 760                 765

Val Lys Val Lys Phe Leu Tyr Glu Asp Lys Met Ala Arg Val Gln Ile
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  Met Ala Pro Ser Ile Ser Lys Thr Val Glu Leu Asn Ser Phe Gly Leu
    1               5                  10                  15

gtc aac ggt aat ttg cct ttg tcc ata acc cta gaa gga tca aat ttc   157
Val Asn Gly Asn Leu Pro Leu Ser Ile Thr Leu Glu Gly Ser Asn Phe
             20                  25                  30

ctc gcc aac ggc cac cct ttt ctc acg gaa gtt ccc gaa aac ata ata   205
Leu Ala Asn Gly His Pro Phe Leu Thr Glu Val Pro Glu Asn Ile Ile
         35                  40                  45

gtc acc cct tca ccc atc gac gcc aag agt agt aag aac aac gag gac   253
Val Thr Pro Ser Pro Ile Asp Ala Lys Ser Ser Lys Asn Asn Glu Asp
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gac gac gtc gta ggt tgc ttc gtg ggc ttc cac gcg gac gag ccc aga   301
Asp Asp Val Val Gly Cys Phe Val Gly Phe His Ala Asp Glu Pro Arg
 65                  70                  75                  80

agc cga cac gtg gct tcc ctg ggg aag ctc aga gga ata aaa ttc atg   349
Ser Arg His Val Ala Ser Leu Gly Lys Leu Arg Gly Ile Lys Phe Met
                85                  90                  95

agc ata ttc cgg ttt aag gtg tgg tgg acc act cac tgg gtc ggt agc   397
Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Ser
            100                 105                 110

aac gga cac gaa ctg gag cac gag aca cag atg atg ctt ctc gac aaa   445
Asn Gly His Glu Leu Glu His Glu Thr Gln Met Met Leu Leu Asp Lys
        115                 120                 125

aac gac cag ctc gga cgc ccc ttt gtg ttg att ctc ccg atc ctc caa   493
Asn Asp Gln Leu Gly Arg Pro Phe Val Leu Ile Leu Pro Ile Leu Gln
    130                 135                 140

gcc tcg ttc cga gcc tcc ctg caa ccc ggt ttg gat gat tac gtg gac   541
Ala Ser Phe Arg Ala Ser Leu Gln Pro Gly Leu Asp Asp Tyr Val Asp
145                 150                 155                 160

gtt tgc atg gag agc ggg tcg aca cgt gtc tgt ggc tcc agc ttc ggg   589
Val Cys Met Glu Ser Gly Ser Thr Arg Val Cys Gly Ser Ser Phe Gly
                165                 170                 175

agc tgc tta tac gtc cac gtt ggc cat gac ccg tat cag ttg ctt aga   637
Ser Cys Leu Tyr Val His Val Gly His Asp Pro Tyr Gln Leu Leu Arg
            180                 185                 190

gaa gca act aaa gtc gtt agg atg cat ttg ggg acg ttc aag ctt ctc   685
Glu Ala Thr Lys Val Val Arg Met His Leu Gly Thr Phe Lys Leu Leu
        195                 200                 205

gag gag aaa acc gcg cca gtg atc ata gac aag ttt ggt tgg tgt aca   733
Glu Glu Lys Thr Ala Pro Val Ile Ile Asp Lys Phe Gly Trp Cys Thr
    210                 215                 220

tgg gac gcg ttt tac ttg aag gtg cat ccc tca ggt gtg tgg gaa ggg   781
Trp Asp Ala Phe Tyr Leu Lys Val His Pro Ser Gly Val Trp Glu Gly
225                 230                 235                 240

gtg aaa ggg ttg gtg gag gga ggg tgc cct cca ggg atg gtc cta atc   829
Val Lys Gly Leu Val Glu Gly Gly Cys Pro Pro Gly Met Val Leu Ile
                245                 250                 255

gac gac ggg tgg caa gcc att tgt cac gac gag gac ccc ata acg gac   877
Asp Asp Gly Trp Gln Ala Ile Cys His Asp Glu Asp Pro Ile Thr Asp
            260                 265                 270

caa gag ggt atg aag cga acc tcc gca ggg gag caa atg cca tgc agg   925
Gln Glu Gly Met Lys Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg
        275                 280                 285

ttg gtg aag ttg gag gaa aat tac aag ttc aga cag tat tgt agt gga   973
Leu Val Lys Leu Glu Glu Asn Tyr Lys Phe Arg Gln Tyr Cys Ser Gly
    290                 295                 300
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aag gat tct gag aag ggt atg ggt gcc ttt gtt agg gac ttg aag gaa   1021
Lys Asp Ser Glu Lys Gly Met Gly Ala Phe Val Arg Asp Leu Lys Glu
305                 310                 315                 320

cag ttt agg agc gtg gag cag gtg tat gtg tgg cac gcg ctt tgt ggg   1069
Gln Phe Arg Ser Val Glu Gln Val Tyr Val Trp His Ala Leu Cys Gly
                325                 330                 335

tat tgg ggt ggg gtc aga ccc aag gtt ccg ggc atg ccc cag gct aag   1117
Tyr Trp Gly Gly Val Arg Pro Lys Val Pro Gly Met Pro Gln Ala Lys
            340                 345                 350

gtt gtc act ccg aag ctg tcc aat gga cta aaa ttg aca atg aag gat   1165
Val Val Thr Pro Lys Leu Ser Asn Gly Leu Lys Leu Thr Met Lys Asp
        355                 360                 365

tta gcg gtg gat aag atc gtc agt aac gga gtt gga ctg gtg cca cca   1213
Leu Ala Val Asp Lys Ile Val Ser Asn Gly Val Gly Leu Val Pro Pro
    370                 375                 380

cac ctg gct cac ctt ttg tac gag ggg ctc cac tcc cgt ttg gaa tct   1261
His Leu Ala His Leu Leu Tyr Glu Gly Leu His Ser Arg Leu Glu Ser
385                 390                 395                 400

gcg ggt att gac ggt gtt aag gtt gac gtt ata cac ttg ctc gag atg   1309
Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Met
                405                 410                 415

cta tcc gag gaa tac ggt ggc cgt gtt gag cta gcc aaa gct tat tac   1357
Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Lys Ala Tyr Tyr
            420                 425                 430

aaa gcg ctc act gct tcg gtg aag aag cat ttc aaa ggc aat ggg gtc   1405
Lys Ala Leu Thr Ala Ser Val Lys Lys His Phe Lys Gly Asn Gly Val
        435                 440                 445

att gcg agc atg gag cat tgt aat gac ttc ttt ctc ctt ggt acc gaa   1453
Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu
    450                 455                 460

gcc ata gcc ctt ggg cgc gta gga gat gat ttt tgg tgc act gat ccc   1501
Ala Ile Ala Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro
465                 470                 475                 480

tct gga gat cca aat ggc acg tat tgg ctc caa ggg tgt cac atg gtg   1549
Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val
                485                 490                 495

cac tgt gcc tac aac agc ttg tgg atg ggg aat ttt att cag ccg gat   1597
His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp
            500                 505                 510

tgg gac atg ttc cag tcc act cac cct tgt gcc gaa ttc cat gcn gcc   1645
Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala
        515                 520                 525

tct agg gcc atc tct ggt gga cca gtt tac gtt agt gat tgt gtt gga   1693
Ser Arg Ala Ile Ser Gly Gly Pro Val Tyr Val Ser Asp Cys Val Gly
    530                 535                 540
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aag cac aac ttc aag ttg ctc aag agc ctc gct ttg cct gat ggg acg   1741
Lys His Asn Phe Lys Leu Leu Lys Ser Leu Ala Leu Pro Asp Gly Thr
545                 550                 555                 560

att ttg cgt tgt caa cac tat gca ctc ccc aca cga gac tgt ttg ttt   1789
Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe
                565                 570                 575

gaa gac ccc ttg cat gat ggg aag aca atg ctc aaa att tgg aat ctc   1837
Glu Asp Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu
            580                 585                 590

aac aaa tat aca ggt gtt ttg ggt cta ttt aat tgc caa gga ggt ggg   1885
Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly
        595                 600                 605

tgg tgt ccc gta act agg aga aac aag agt gcc tct gaa ttt tca caa   1933
Trp Cys Pro Val Thr Arg Arg Asn Lys Ser Ala Ser Glu Phe Ser Gln
    610                 615                 620

act gtg aca tgc tta gcg agt cct caa gac att gaa tgg agc aat ggg   1981
Thr Val Thr Cys Leu Ala Ser Pro Gln Asp Ile Glu Trp Ser Asn Gly
625                 630                 635                 640

aaa agc cca ata tgc ata aaa ggg atg aat gtg ttt gct gta tat ttg   2029
Lys Ser Pro Ile Cys Ile Lys Gly Met Asn Val Phe Ala Val Tyr Leu
                645                 650                 655

ttc aag gac cac aaa cta aag ctc atg aag gca tca gag aaa ttg gaa   2077
Phe Lys Asp His Lys Leu Lys Leu Met Lys Ala Ser Glu Lys Leu Glu
            660                 665                 670

gtt tca ctt gag cca ttt act ttt gag cta ttg aca gtg tct cca gtg   2125
Val Ser Leu Glu Pro Phe Thr Phe Glu Leu Leu Thr Val Ser Pro Val
        675                 680                 685

att gtg ctg tca aaa aag tta att caa ttt gct cca att gga tta gtg   2173
Ile Val Leu Ser Lys Lys Leu Ile Gln Phe Ala Pro Ile Gly Leu Val
    690                 695                 700

aac atg ctt aac act ggt ggt gcc att cag tcc atg gag ttt gac aac   2221
Asn Met Leu Asn Thr Gly Gly Ala Ile Gln Ser Met Glu Phe Asp Asn
705                 710                 715                 720

cac ata gat gtg gtc aaa att ggg gtt agg ggt tgt ggg gag atg aag   2269
His Ile Asp Val Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Lys
                725                 730                 735

gtg ttt gca tca gag aaa cca gtt agt tgc aaa cta gat ggg gta gtt   2317
Val Phe Ala Ser Glu Lys Pro Val Ser Cys Lys Leu Asp Gly Val Val
            740                 745                 750

gta aaa ttt gat tat gag gat aaa atg ctg aga gtg caa gtt ccc tgg   2365
Val Lys Phe Asp Tyr Glu Asp Lys Met Leu Arg Val Gln Val Pro Trp
        755                 760                 765

cct agt gct tca aaa ttg tca atg gtt gag ttt tta ttt tgatccctga   2414
Pro Ser Ala Ser Lys Leu Ser Met Val Glu Phe Leu Phe
    770                 775                 780

aggtgaattt gggatactat gatgtttgac tctcttttta agtaataaga gtcatatttt 2474
```

tctgttgtaa aaaaaaaaaa aaaa 2498

<210> 4
<211> 781
<212> PRT
<213> Glycine max

<400> 4

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Met Ala Pro Ser Ile Ser Lys Thr Val Glu Leu Asn Ser Phe Gly Leu
  1               5                  10                  15

Val Asn Gly Asn Leu Pro Leu Ser Ile Thr Leu Glu Gly Ser Asn Phe
             20                  25                  30

Leu Ala Asn Gly His Pro Phe Leu Thr Glu Val Pro Glu Asn Ile Ile
         35                  40                  45

Val Thr Pro Ser Pro Ile Asp Ala Lys Ser Ser Lys Asn Asn Glu Asp
     50                  55                  60

Asp Asp Val Val Gly Cys Phe Val Gly Phe His Ala Asp Glu Pro Arg
 65                  70                  75                  80

Ser Arg His Val Ala Ser Leu Gly Lys Leu Arg Gly Ile Lys Phe Met
                 85                  90                  95

Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Ser
            100                 105                 110

Asn Gly His Glu Leu Glu His Glu Thr Gln Met Met Leu Leu Asp Lys
        115                 120                 125

Asn Asp Gln Leu Gly Arg Pro Phe Val Leu Ile Leu Pro Ile Leu Gln
    130                 135                 140

Ala Ser Phe Arg Ala Ser Leu Gln Pro Gly Leu Asp Asp Tyr Val Asp
145                 150                 155                 160

Val Cys Met Glu Ser Gly Ser Thr Arg Val Cys Gly Ser Ser Phe Gly
                165                 170                 175

Ser Cys Leu Tyr Val His Val Gly His Asp Pro Tyr Gln Leu Leu Arg
            180                 185                 190

Glu Ala Thr Lys Val Val Arg Met His Leu Gly Thr Phe Lys Leu Leu
        195                 200                 205

Glu Glu Lys Thr Ala Pro Val Ile Ile Asp Lys Phe Gly Trp Cys Thr
    210                 215                 220

Trp Asp Ala Phe Tyr Leu Lys Val His Pro Ser Gly Val Trp Glu Gly
225                 230                 235                 240

Val Lys Gly Leu Val Glu Gly Gly Cys Pro Pro Gly Met Val Leu Ile
                245                 250                 255

Asp Asp Gly Trp Gln Ala Ile Cys His Asp Glu Asp Pro Ile Thr Asp
            260                 265                 270
```

```
Gln Glu Gly Met Lys Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg
        275                 280                 285

Leu Val Lys Leu Glu Glu Asn Tyr Lys Phe Arg Gln Tyr Cys Ser Gly
    290                 295                 300

Lys Asp Ser Glu Lys Gly Met Gly Ala Phe Val Arg Asp Leu Lys Glu
305                 310                 315                 320

Gln Phe Arg Ser Val Glu Gln Val Tyr Val Trp His Ala Leu Cys Gly
                325                 330                 335

Tyr Trp Gly Gly Val Arg Pro Lys Val Pro Gly Met Pro Gln Ala Lys
            340                 345                 350

Val Val Thr Pro Lys Leu Ser Asn Gly Leu Lys Leu Thr Met Lys Asp
        355                 360                 365

Leu Ala Val Asp Lys Ile Val Ser Asn Gly Val Gly Leu Val Pro Pro
    370                 375                 380

His Leu Ala His Leu Leu Tyr Glu Gly Leu His Ser Arg Leu Glu Ser
385                 390                 395                 400

Ala Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu Glu Met
                405                 410                 415

Leu Ser Glu Glu Tyr Gly Gly Arg Val Glu Leu Ala Lys Ala Tyr Tyr
            420                 425                 430

Lys Ala Leu Thr Ala Ser Val Lys Lys His Phe Lys Gly Asn Gly Val
        435                 440                 445

Ile Ala Ser Met Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu
    450                 455                 460

Ala Ile Ala Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro
465                 470                 475                 480

Ser Gly Asp Pro Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val
                485                 490                 495

His Cys Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp
            500                 505                 510

Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala
        515                 520                 525

Ser Arg Ala Ile Ser Gly Gly Pro Val Tyr Val Ser Asp Cys Val Gly
    530                 535                 540

Lys His Asn Phe Lys Leu Leu Lys Ser Leu Ala Leu Pro Asp Gly Thr
545                 550                 555                 560

Ile Leu Arg Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe
                565                 570                 575

Glu Asp Pro Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu
            580                 585                 590

Asn Lys Tyr Thr Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly
```

```
        595                 600                 605

Trp Cys Pro Val Thr Arg Arg Asn Lys Ser Ala Ser Glu Phe Ser Gln
    610                 615                 620

Thr Val Thr Cys Leu Ala Ser Pro Gln Asp Ile Glu Trp Ser Asn Gly
625                 630                 635                 640

Lys Ser Pro Ile Cys Ile Lys Gly Met Asn Val Phe Ala Val Tyr Leu
                645                 650                 655

Phe Lys Asp His Lys Leu Lys Leu Met Lys Ala Ser Glu Lys Leu Glu
            660                 665                 670

Val Ser Leu Glu Pro Phe Thr Phe Glu Leu Leu Thr Val Ser Pro Val
        675                 680                 685

Ile Val Leu Ser Lys Lys Leu Ile Gln Phe Ala Pro Ile Gly Leu Val
    690                 695                 700

Asn Met Leu Asn Thr Gly Gly Ala Ile Gln Ser Met Glu Phe Asp Asn
705                 710                 715                 720

His Ile Asp Val Val Lys Ile Gly Val Arg Gly Cys Gly Glu Met Lys
                725                 730                 735

Val Phe Ala Ser Glu Lys Pro Val Ser Cys Lys Leu Asp Gly Val Val
            740                 745                 750

Val Lys Phe Asp Tyr Glu Asp Lys Met Leu Arg Val Gln Val Pro Trp
        755                 760                 765

Pro Ser Ala Ser Lys Leu Ser Met Val Glu Phe Leu Phe
    770                 775                 780


<210> 5
<211> 1762
<212> DNA
<213> Stachys sieboldii

<220>
<221> CDS
<222> (2)..(1759)

<400> 5
g aca aac ggg tcg gat ctt gag cgg gaa act caa ata gtc gtg ctc gac 49
  Thr Asn Gly Ser Asp Leu Glu Arg Glu Thr Gln Ile Val Val Leu Asp
    1               5                  10                  15

aag tcc gac gac agg ccc tac atc gtg ctg ctt ccg ctc atc gag ggg   97
Lys Ser Asp Asp Arg Pro Tyr Ile Val Leu Leu Pro Leu Ile Glu Gly
            20                  25                  30

cag ttt cgg gct tcc ctt cag ccc ggt gtg gat gat ttt atc gat att   145
Gln Phe Arg Ala Ser Leu Gln Pro Gly Val Asp Asp Phe Ile Asp Ile
        35                  40                  45

tgt gtc gaa agc ggg tca acc aag gtc aac gag tcc tcg ttc cgt gct   193
Cys Val Glu Ser Gly Ser Thr Lys Val Asn Glu Ser Ser Phe Arg Ala
    50                  55                  60
```

```
tcg ctc tac atg cac gcc ggt gat gac cct ttt acc ctg gtg aag gac   241
Ser Leu Tyr Met His Ala Gly Asp Asp Pro Phe Thr Leu Val Lys Asp
 65                  70                  75                  80

gcc gtg aag gtg gcg cgc cac cac ctc ggg acg ttc agg ctg ctg gag   289
Ala Val Lys Val Ala Arg His His Leu Gly Thr Phe Arg Leu Leu Glu
                 85                  90                  95

gag aaa act ccg ccg ggg atc gtc gac aaa ttc ggg tgg tgc acg tgg   337
Glu Lys Thr Pro Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp
            100                 105                 110

gat gcg ttc tac ctc aac gtc cag ccc cac ggc gtt atg gag ggc gtg   385
Asp Ala Phe Tyr Leu Asn Val Gln Pro His Gly Val Met Glu Gly Val
        115                 120                 125

cag ggg ctg gtt gac ggc gga tgt ccg ccg ggg ctg gtg ttg atc gac   433
Gln Gly Leu Val Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp
    130                 135                 140

gac ggg tgg cag tcc att tgt cac gac aac gac gcg ctc acc acc gag   481
Asp Gly Trp Gln Ser Ile Cys His Asp Asn Asp Ala Leu Thr Thr Glu
145                 150                 155                 160

ggg atg ggg aga acc tcc gcc gga gag caa atg ccc tgc agg ttg atc   529
Gly Met Gly Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Ile
                165                 170                 175

aag ttt gag gag aat tac aag ttc agg gag tac gag agc ccg aat aaa   577
Lys Phe Glu Glu Asn Tyr Lys Phe Arg Glu Tyr Glu Ser Pro Asn Lys
            180                 185                 190

act ggg ccg ggc ccg aat acg ggg atg ggg gcc ttt att cgt gac atg   625
Thr Gly Pro Gly Pro Asn Thr Gly Met Gly Ala Phe Ile Arg Asp Met
        195                 200                 205

aag gac aat ttc aag agt gtg gac tac gtg tac gtg tgg cat gcg ttg   673
Lys Asp Asn Phe Lys Ser Val Asp Tyr Val Tyr Val Trp His Ala Leu
    210                 215                 220

tgt ggt tat tgg ggc ggg ctc agg ccc aat gtt ccg ggc ctg ccc gag   721
Cys Gly Tyr Trp Gly Gly Leu Arg Pro Asn Val Pro Gly Leu Pro Glu
225                 230                 235                 240

gct aag ctc att gag ccc aaa ctg act cct ggg ctt aag acc acc atg   769
Ala Lys Leu Ile Glu Pro Lys Leu Thr Pro Gly Leu Lys Thr Thr Met
                245                 250                 255

gaa gat ttg gct gtt gat aag att gtc aac aat ggc gtg ggt ctg gtc   817
Glu Asp Leu Ala Val Asp Lys Ile Val Asn Asn Gly Val Gly Leu Val
            260                 265                 270

cca ccg gag ttt gtt gaa caa atg tat gaa gga tta cat tca cat ctc   865
Pro Pro Glu Phe Val Glu Gln Met Tyr Glu Gly Leu His Ser His Leu
        275                 280                 285

gaa tct gtg ggg att gat gga gtc aaa gtt gac gtc atc cat ttg ttg   913
Glu Ser Val Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu
    290                 295                 300
```

```
gaa atg ttg tgt gaa gac tat ggt ggg aga gtg gac tta gcc aag gct   961
Glu Met Leu Cys Glu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala
305                 310                 315                 320

tat tac aag gcc tta tca agc tca gtt aac aac cac ttc aac ggc aac  1009
Tyr Tyr Lys Ala Leu Ser Ser Ser Val Asn Asn His Phe Asn Gly Asn
                325                 330                 335

ggc gtc atc gct ggc ctg gag cac tgc aat gac ttc atg ttt ctc gga  1057
Gly Val Ile Ala Gly Leu Glu His Cys Asn Asp Phe Met Phe Leu Gly
            340                 345                 350

acc gag gcc att acc ttg ggt cgt gtc ggg gat gat ttt tgg tgc act  1105
Thr Glu Ala Ile Thr Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr
        355                 360                 365

gat cca tct gga gat ccc aat ggc acg ttc tgg ttg caa ggg tgt cac  1153
Asp Pro Ser Gly Asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His
    370                 375                 380

atg gtg cac tgc gcc tac aac agc ata tgg atg ggt aat ttc atc cac  1201
Met Val His Cys Ala Tyr Asn Ser Ile Trp Met Gly Asn Phe Ile His
385                 390                 395                 400

cct gat tgg gac atg ttt caa tcg act cac cct tgc gct gaa ttc cac  1249
Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His
                405                 410                 415

gct gcc tca cga gcc atc tcc ggc ggg ccc att tac gtc agt gac tcg  1297
Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser
            420                 425                 430

gtc gga aag cac aac ttc gag ctc ctt agg agc ctc gtt ctt ccc gat  1345
Val Gly Lys His Asn Phe Glu Leu Leu Arg Ser Leu Val Leu Pro Asp
        435                 440                 445

ggc tcc atc ctc cgt tgt gat tac tac gcg ctt ccg act cgc gat tgc  1393
Gly Ser Ile Leu Arg Cys Asp Tyr Tyr Ala Leu Pro Thr Arg Asp Cys
    450                 455                 460

ctc ttt gaa gat cca ctt cac aat ggc aag act atg ctc aaa att tgg  1441
Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp
465                 470                 475                 480

aat tat aac aag ttc acc gga gtt gtc gga act ttc aac tgc caa ggt  1489
Asn Tyr Asn Lys Phe Thr Gly Val Val Gly Thr Phe Asn Cys Gln Gly
                485                 490                 495

ggc ggg tgg agc cgg gaa gtg cgt cgc aac caa tgc gct gcc gag tat  1537
Gly Gly Trp Ser Arg Glu Val Arg Arg Asn Gln Cys Ala Ala Glu Tyr
            500                 505                 510

tcc cac gcc gtc tcc tct agc gct ggt ccg agt gac att gag tgg aag  1585
Ser His Ala Val Ser Ser Ser Ala Gly Pro Ser Asp Ile Glu Trp Lys
        515                 520                 525

caa gga acg agt ccg atc gac gtc gac ggc gtc aaa aca ttc gcg ttg  1633
Gln Gly Thr Ser Pro Ile Asp Val Asp Gly Val Lys Thr Phe Ala Leu
    530                 535                 540

tac cta ttc cac gag aag aaa ctc gtc ctt tct aag cca tca gac aaa  1681
```

```
Tyr Leu Phe His Glu Lys Lys Leu Val Leu Ser Lys Pro Ser Asp Lys
545                 550                 555                 560

atc gac atc acg ctt gag ccc ttc gat ttt gag ctg ata acc gtt tct   1729
Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val Ser
                565                 570                 575

cca gtc aaa act cta gcc aat tgc acc gtc caa                       1762
Pro Val Lys Thr Leu Ala Asn Cys Thr Val
            580                 585


<210> 6
<211> 586
<212> PRT
<213> Stachys sieboldii

<400> 6
Thr Asn Gly Ser Asp Leu Glu Arg Glu Thr Gln Ile Val Val Leu Asp
  1               5                  10                  15

Lys Ser Asp Asp Arg Pro Tyr Ile Val Leu Leu Pro Leu Ile Glu Gly
             20                  25                  30

Gln Phe Arg Ala Ser Leu Gln Pro Gly Val Asp Asp Phe Ile Asp Ile
         35                  40                  45

Cys Val Glu Ser Gly Ser Thr Lys Val Asn Glu Ser Ser Phe Arg Ala
     50                  55                  60

Ser Leu Tyr Met His Ala Gly Asp Asp Pro Phe Thr Leu Val Lys Asp
 65                  70                  75                  80

Ala Val Lys Val Ala Arg His His Leu Gly Thr Phe Arg Leu Leu Glu
                 85                  90                  95

Glu Lys Thr Pro Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp
            100                 105                 110

Asp Ala Phe Tyr Leu Asn Val Gln Pro His Gly Val Met Glu Gly Val
        115                 120                 125

Gln Gly Leu Val Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp
    130                 135                 140

Asp Gly Trp Gln Ser Ile Cys His Asp Asn Asp Ala Leu Thr Thr Glu
145                 150                 155                 160

Gly Met Gly Arg Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Ile
                165                 170                 175

Lys Phe Glu Glu Asn Tyr Lys Phe Arg Glu Tyr Glu Ser Pro Asn Lys
            180                 185                 190

Thr Gly Pro Gly Pro Asn Thr Gly Met Gly Ala Phe Ile Arg Asp Met
        195                 200                 205

Lys Asp Asn Phe Lys Ser Val Asp Tyr Val Tyr Val Trp His Ala Leu
    210                 215                 220

Cys Gly Tyr Trp Gly Gly Leu Arg Pro Asn Val Pro Gly Leu Pro Glu
```

225 230 235 240

Ala Lys Leu Ile Glu Pro Lys Leu Thr Pro Gly Leu Lys Thr Thr Met
245 250 255

Glu Asp Leu Ala Val Asp Lys Ile Val Asn Asn Gly Val Gly Leu Val
260 265 270

Pro Pro Glu Phe Val Glu Gln Met Tyr Glu Gly Leu His Ser His Leu
275 280 285

Glu Ser Val Gly Ile Asp Gly Val Lys Val Asp Val Ile His Leu Leu
290 295 300

Glu Met Leu Cys Glu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala
305 310 315 320

Tyr Tyr Lys Ala Leu Ser Ser Ser Val Asn Asn His Phe Asn Gly Asn
325 330 335

Gly Val Ile Ala Gly Leu Glu His Cys Asn Asp Phe Met Phe Leu Gly
340 345 350

Thr Glu Ala Ile Thr Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr
355 360 365

Asp Pro Ser Gly Asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His
370 375 380

Met Val His Cys Ala Tyr Asn Ser Ile Trp Met Gly Asn Phe Ile His
385 390 395 400

Pro Asp Trp Asp Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His
405 410 415

Ala Ala Ser Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser
420 425 430

Val Gly Lys His Asn Phe Glu Leu Leu Arg Ser Leu Val Leu Pro Asp
435 440 445

Gly Ser Ile Leu Arg Cys Asp Tyr Tyr Ala Leu Pro Thr Arg Asp Cys
450 455 460

Leu Phe Glu Asp Pro Leu His Asn Gly Lys Thr Met Leu Lys Ile Trp
465 470 475 480

Asn Tyr Asn Lys Phe Thr Gly Val Val Gly Thr Phe Asn Cys Gln Gly
485 490 495

Gly Gly Trp Ser Arg Glu Val Arg Arg Asn Gln Cys Ala Ala Glu Tyr
500 505 510

Ser His Ala Val Ser Ser Ser Ala Gly Pro Ser Asp Ile Glu Trp Lys
515 520 525

Gln Gly Thr Ser Pro Ile Asp Val Asp Gly Val Lys Thr Phe Ala Leu
530 535 540

Tyr Leu Phe His Glu Lys Lys Leu Val Leu Ser Lys Pro Ser Asp Lys
545 550 555 560

```
Ile Asp Ile Thr Leu Glu Pro Phe Asp Phe Glu Leu Ile Thr Val Ser
                565                 570                 575

Pro Val Lys Thr Leu Ala Asn Cys Thr Val
            580                 585
```

<210> 7
<211> 993
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (2)..(814)

<400> 7

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c cag tcc acg cac ccc tgc gcc gcc ttc cac gcc gcg tcc cgc gcc atc 49
  Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg Ala Ile
    1               5                  10                  15

tcc ggc ggg ccc atc tac gtc agc gac tcg gtg ggg cag cac gac ttc   97
Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Gln His Asp Phe
            20                  25                  30

gcg ctg ctc cgc cgc ctg gcg ctc ccc gac ggc acc gtc ctc cgg tgc   145
Ala Leu Leu Arg Arg Leu Ala Leu Pro Asp Gly Thr Val Leu Arg Cys
        35                  40                  45

gag ggc cac gcg ctg ccc acg cgc gac tgc ctc ttc gcc gac ccg ctc   193
Glu Gly His Ala Leu Pro Thr Arg Asp Cys Leu Phe Ala Asp Pro Leu
    50                  55                  60

cac gac ggc cgg acc gtg ctc aag atc tgg aac gtg aac cgc ttc gcc   241
His Asp Gly Arg Thr Val Leu Lys Ile Trp Asn Val Asn Arg Phe Ala
65                  70                  75                  80

ggc gtc gtc ggc gcc ttc aac tgc cag ggc ggc ggg tgg agc ccc gag   289
Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro Glu
                85                  90                  95

gcg cgg cgg aac aag tgc ttc tcg gag ttc tcc gtg ccc ctg gcc gcg   337
Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala Ala
            100                 105                 110

cgc gcc tcg ccg tcc gac gtc gag tgg aag agc ggc aag gcg ggg cca   385
Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly Pro
        115                 120                 125

ggc gtc agc gtc aag gac gtc tcc cag ttc gcc gtg tac gcg gtc gag   433
Gly Val Ser Val Lys Asp Val Ser Gln Phe Ala Val Tyr Ala Val Glu
    130                 135                 140

gcc agg acg ctg cag ctg ctg cgc ccc gac gag ggc gtc gac ctc acg   481
Ala Arg Thr Leu Gln Leu Leu Arg Pro Asp Glu Gly Val Asp Leu Thr
145                 150                 155                 160

ctg cag ccc ttc acc tac gag ctc ttc gtc gtt gcc ccc gtg cgc gtc   529
Leu Gln Pro Phe Thr Tyr Glu Leu Phe Val Val Ala Pro Val Arg Val
                165                 170                 175
```

```
atc tcg cat gag cgg gcc atc aag ttc gcg ccc atc gga ctc gcc aac   577
Ile Ser His Glu Arg Ala Ile Lys Phe Ala Pro Ile Gly Leu Ala Asn
            180                 185                 190

atg ctc aac acc gcc ggc gcc gtg cag gcg ttc gag gcc aag aaa gat   625
Met Leu Asn Thr Ala Gly Ala Val Gln Ala Phe Glu Ala Lys Lys Asp
        195                 200                 205

gct agc ggc gtc acg gca gag gtg ttc gtg aag ggc gca ggg gag ctg   673
Ala Ser Gly Val Thr Ala Glu Val Phe Val Lys Gly Ala Gly Glu Leu
    210                 215                 220

gtg gcg tac tcg tcg gcg acg ccc agg ctc tgc aag gtg aac ggc gac   721
Val Ala Tyr Ser Ser Ala Thr Pro Arg Leu Cys Lys Val Asn Gly Asp
225                 230                 235                 240

gag gcc gag ttc acg tac aag gac ggc gtg gtc acc gtc gac gtg ccg   769
Glu Ala Glu Phe Thr Tyr Lys Asp Gly Val Val Thr Val Asp Val Pro
                245                 250                 255

tgg tcg ggg tcg tcg tcg aag ctg tgt tgc gtc cag tac gtc tac       814
Trp Ser Gly Ser Ser Ser Lys Leu Cys Cys Val Gln Tyr Val Tyr
            260                 265                 270

tgagccggac gggccgatga ctctgcgtct ctgctccctg ctggcctgct caggacataa 874

tctaatgttt agagcttacc aggttttaca gctctatcag tttacttttg tttttctgct 934

cttcgttttt taagaattat ttctattgtg tgaattaatg agtgctttcc ttctaaaaa  993
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<210> 8
<211> 271
<212> PRT
<213> Zea mays

<400> 8

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Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg Ala Ile
  1               5                  10                  15

Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Gln His Asp Phe
             20                  25                  30

Ala Leu Leu Arg Arg Leu Ala Leu Pro Asp Gly Thr Val Leu Arg Cys
         35                  40                  45

Glu Gly His Ala Leu Pro Thr Arg Asp Cys Leu Phe Ala Asp Pro Leu
     50                  55                  60

His Asp Gly Arg Thr Val Leu Lys Ile Trp Asn Val Asn Arg Phe Ala
 65                  70                  75                  80

Gly Val Val Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Ser Pro Glu
                 85                  90                  95

Ala Arg Arg Asn Lys Cys Phe Ser Glu Phe Ser Val Pro Leu Ala Ala
            100                 105                 110

Arg Ala Ser Pro Ser Asp Val Glu Trp Lys Ser Gly Lys Ala Gly Pro
        115                 120                 125
```

```
Gly Val Ser Val Lys Asp Val Ser Gln Phe Ala Val Tyr Ala Val Glu
    130                 135                 140

Ala Arg Thr Leu Gln Leu Leu Arg Pro Asp Glu Gly Val Asp Leu Thr
145                 150                 155                 160

Leu Gln Pro Phe Thr Tyr Glu Leu Phe Val Val Ala Pro Val Arg Val
                165                 170                 175

Ile Ser His Glu Arg Ala Ile Lys Phe Ala Pro Ile Gly Leu Ala Asn
            180                 185                 190

Met Leu Asn Thr Ala Gly Ala Val Gln Ala Phe Glu Ala Lys Lys Asp
        195                 200                 205

Ala Ser Gly Val Thr Ala Glu Val Phe Val Lys Gly Ala Gly Glu Leu
    210                 215                 220

Val Ala Tyr Ser Ser Ala Thr Pro Arg Leu Cys Lys Val Asn Gly Asp
225                 230                 235                 240

Glu Ala Glu Phe Thr Tyr Lys Asp Gly Val Val Thr Val Asp Val Pro
                245                 250                 255

Trp Ser Gly Ser Ser Ser Lys Leu Cys Cys Val Gln Tyr Val Tyr
            260                 265                 270
```

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer 1 (from list 1)

<400> 9
aattttcaag catagccaag ttaaccacct 30

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer 2 (from list 1)

<400> 10
gctcacaaga taatgatgtt agtc 24

<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
primer 3 (from list 1)

<400> 11
atacaagtga ggaacttgac ca 22

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 4 (from list 1)

<400> 12
ccaaaccata gcaaacctaa gcac 24

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 5 (from list 1)

<400> 13
acaacagaaa aatatgactc ttattact 28

<210> 14
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 6 (from list 1)

<400> 14
aaaagagagt caaacatcat agtatc 26

<210> 15
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 1 (from list 2)

<400> 15
atggcaccac caagcataac caaaactgc 29

<210> 16
<211> 43

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 2 (from list 2)

<400> 16
atggcaccac caagcataac caaaactgca accctccaag acg 43

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 3 (from list 2)

<400> 17
tcaaaataaa aactggacca aagac 25

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 4 (from list 2)

<400> 18
tcaaaataaa aactggacca aagacaatgt 30

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 5 (from list 2)

<400> 19
atggctccaa gcataagcaa aactg 25

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 6 (from list 2)

<400> 20
atggctccaa gcataagcaa aactgtggaa ct 32

<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 7 (from list 2)

<400> 21
tcaaaataaa aactcaacca ttgac 25

<210> 22
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 8 (from list 2)

<400> 22
tcaaaataaa aactcaacca ttgacaattt tgaagcact 39

<210> 23
<211> 20
<212> PRT
<213> Vicia faba

<400> 23
Gly Ile Lys Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp Thr Thr
1 5 10 15

His Trp Val Gly
20

<210> 24
<211> 14
<212> PRT
<213> Vicia faba

<400> 24
Ile Ile Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr
1 5 10

<210> 25
<211> 15
<212> PRT
<213> Vicia faba

<400> 25
Gly Gly Cys Pro Pro Gly Phe Val Ile Ile Asp Asp Gly Trp Gln
1 5 10 15

<210> 26
<211> 17
<212> PRT
<213> Vicia faba

<400> 26
Thr Ser Ala Gly Glu Gln Met Pro Cys Arg Leu Val Lys Tyr Glu Glu
1 5 10 15

Asn

<210> 27
<211> 16
<212> PRT
<213> Vicia faba

<400> 27
Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp Gly Gly Val Arg Pro
1 5 10 15

<210> 28
<211> 20
<212> PRT
<213> Vicia faba

<400> 28
Thr Met Glu Asp Leu Ala Val Asp Lys Ile Val Glu Asn Gly Val Gly
1 5 10 15

Leu Val Pro Pro
20

<210> 29
<211> 23
<212> PRT
<213> Vicia faba

<400> 29
Gly Leu His Ser His Leu Glu Ser Ala Gly Ile Asp Gly Val Lys Val
1 5 10 15

Asp Val Ile His Leu Leu Glu
20

<210> 30
<211> 14
<212> PRT
<213> Vicia faba

<400> 30
Gly Gly Arg Val Glu Leu Ala Arg Ala Tyr Tyr Lys Ala Leu
1 5 10

<210> 31
<211> 12

<212> PRT
<213> Vicia faba

<400> 31
Val Lys Lys His Phe Lys Gly Asn Gly Val Ile Ala
1 5 10

<210> 32
<211> 46
<212> PRT
<213> Vicia faba

<400> 32
Glu His Cys Asn Asp Phe Phe Leu Leu Gly Thr Glu Ala Ile Ser Leu
1 5 10 15

Gly Arg Val Gly Asp Asp Phe Trp Cys Ser Asp Pro Ser Gly Asp Pro
20 25 30

Asn Gly Thr Tyr Trp Leu Gln Gly Cys His Met Val His Cys
35 40 45

<210> 33
<211> 43
<212> PRT
<213> Vicia faba

<400> 33
Ala Tyr Asn Ser Leu Trp Met Gly Asn Phe Ile Gln Pro Asp Trp Asp
1 5 10 15

Met Phe Gln Ser Thr His Pro Cys Ala Glu Phe His Ala Ala Ser Arg
20 25 30

Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp
35 40

<210> 34
<211> 9
<212> PRT
<213> Vicia faba

<400> 34
Leu Pro Asp Gly Ser Ile Leu Arg Cys
1 5

<210> 35
<211> 24
<212> PRT
<213> Vicia faba

<400> 35
Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp Pro Leu His Asn Gly
1 5 10 15

Lys Thr Met Leu Lys Ile Trp Asn
20

<210> 36
<211> 13
<212> PRT
<213> Vicia faba

<400> 36
Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp
1 5 10

<210> 37
<211> 9
<212> PRT
<213> Vicia faba

<400> 37
Phe Ala Pro Ile Gly Leu Val Asn Met
1 5

<210> 38
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 1-F (from list 4)

<400> 38
ttnaangtnt ggtggacnac ncantgggtn gg 32

<210> 39
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(41)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 2-F (from list 4)

<400> 39
atnatngana anttnggntg gtgnacntgg gangcnttnt a 41

<210> 40
<211> 41
<212> DNA

<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(41)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 2-RV (from list 4)

<400> 40
tanaangcnt cccangtnca ccanccnaan ttntcnatna t 41

<210> 41
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(44)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 3-F (from list 4)

<400> 41
ggnggntgnc cnccnggntt ngtnatnatn ganganggnt ggca 44

<210> 42
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(44)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 3-RV (from list 4)

<400> 42
tgccanccnt cntcnatnat nacnaanccn ggnggncanc cncc 44

<210> 43
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 4-F (from list 4)

<400> 43
aanaancant tnaanggnaa nggngtnatn gc 32

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 4-RV (from list 4)

<400> 44
gcnatnacnc cnttnccntt naantgnttn tt 32

<210> 45
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(38)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 5-F (from list 4)

<400> 45
tggatgggna anttnatnca nccngantgg ganatgtt 38

<210> 46
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(38)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 5-RV (from list 4)

<400> 46
aacatntccc antcnggntg natnaanttn cccatcca 38

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (1)..(27)
<223> n = inosine

<220>
<223> Description of Artificial Sequence:synthetic
primer 6-RV (from list 4)

<400> 47
catnttnacn arnccnatng gngcnaa 27

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 8.2 (from list 5)

<400> 48
aaracngcnc cnagyathat hgacaa 26

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 13.4 (from list 5)

<400> 49
aarathtgga ayctnaacaa 20

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 7.4 (from list 5)

<400> 50
aargcnagrg tngtngtncc naag 24

<210> 51
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 13.3RV (from list 5)

<400> 51
yttrttnagr ttccadattt t 21

<210> 52
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 10.3RV (from list 5)

<400> 52
yttrtcytcr tanagraatt t 21

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RES-2RV (from list 6)

<400> 53
ggctgaggtt cggttcattc ctgaatcatc 30

<210> 54
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-7 (from list 6)

<400> 54
ccaaatggta catattggct ccaaggttgt 30

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-8 (from list 6)

<400> 55
aagagtgtat ctgaattttc acgcgcggtg 30

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-9 (from list 6)

<400> 56
tggtgcaatg ggaaaactcc aatgagcacc 30

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-10 (from list 6)

<400> 57
atgaagtgtt ctgatagatt gaaagtttcg 30

<210> 58
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-11 (from list 6)

<400> 58
cagtctctgg agtttgatga taatgcaagt 30

<210> 59
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-N (from list 7)

<400> 59
cgcggatcca ccatggcacc accaagcata accaaaactg c 41

<210> 60
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer RS-C (from list 7)

<220>
<221> modified_base
<222> (1)..(37)
<223> n = inosine

<400> 60
tgctctagat tatcaaaata aaaactggac caaagac 37

<210> 61
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 1-F (from list 8)

<220>
<221> modified_base
<222> (1)..(35)
<223> n= inosine

<400> 61
cgattnaang tntggtggac nacncantgg gtngg 35

<210> 62
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 2-RV (from list 8)

<220>
<221> modified_base
<222> (1)..(45)
<223> n = inosine

<400> 62
ggcctanaan gcntcccang tncaccancc naanttntcn atnat 45

<210> 63
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 5-F (from list 8)

<220>
<221> modified_base
<222> (1)..(41)
<223> n = inosine

<400> 63

cgatggatgg gnaanttnat ncanccngan tggganatgt t 41

<210> 64
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer 6-RV (from list 8)

<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine

<400> 64
ggccacatnt tnacnarncc natnggngcn aa 32

<210> 65
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer SN-1 (from list 9)

<400> 65
cacgaactgg ggcacgagac acagatgatg 30

<210> 66
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer SC-3RV (from list 9)

<400> 66
aagcaagtca cggagtgtga atagtcagag 30

<210> 67
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer SC-5 (from list 9)

<400> 67
acacgagact gtttgtttga agacccctg 30

<210> 68

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer SC-6 (from list 9)

<400> 68
tggaatctca acaaatatac aggtg 25

<210> 69
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer SN-3RV (from list 9)

<400> 69
gggtcatggc caacgtggac gtataagcac 30

<210> 70
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer SN-4RV (from list 9)

<400> 70
gatgatcact ggcgcggttt tctcctcgag 30

<210> 71
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 1-F (from list 10)

<220>
<221> modified_base
<222> (1)..(35)
<223> n = inosine

<400> 71
cgattnaang tntggtggac nacncantgg gtngg 35

<210> 72
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 4-RV (from list 10)

<220>
<221> modified_base
<222> (1)..(37)
<223> n = inosine

<400> 72
ggccagcnat nacnccnttn ccnttnaant gnttntt 37

<210> 73
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 2-F (from list 10)

<220>
<221> modified_base
<222> (1)..(44)
<223> n = inosine

<400> 73
cgaatnatng anaanttngg ntggtgnacn tgggangcnt tnta 44

<210> 74
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 6-RV (from list 10)

<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine

<400> 74
ggccacatnt tnacnarncc natnggngcn aa 32

<210> 75
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 5-F (from list 11)

<220>
<221> modified_base
<222> (1)..(41)

<223> n= inosine

<400> 75
cgatggatgg gnaanttnat ncanccngan tggganatgt t 41

<210> 76
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer 6-RV (from list 11)

<220>
<221> modified_base
<222> (1)..(32)
<223> n = inosine

<400> 76
ggccacatnt tnacnarncc natnggngcn aa 32

<210> 77
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer M10 (from list 12)

<400> 77
gacgtcgagt ggaagagcgg caagg 25

<210> 78
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer M-11 (from list 12)

<400> 78
cacctacgag ctcttcgtcg ttgcc 25

<210> 79
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
primer BamSac-(+) (from list 13)

<400> 79
gatcgagctc gtgtcggatc cagct 25

<210> 80
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer BamSac-(-) (from list 13)

<400> 80
ggatccgaca cgagctc 17

<210> 81
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer 35S (from list 14)

<400> 81
ttccagtatg gacgattcaa ggcttgcttc 30

<210> 82
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer NOS (from list 14)

<400> 82
atgtataatt gcgggactct aatca 25

<210> 83
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic primer RS-F (from list 14)

<400> 83
aagagtgtat ctgaattttc acgcgcggtg 30

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic

primer RS-RV (from list 14)

<400> 84
accttcccat acacctttg gatgaacctt caa 33

<210> 85
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:BamHI-NcoI linker (from Fig. 1)

<400> 85
ggatccacca tggcaccacc aagcataacc aaaactgc 38

<210> 86
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:XbaI-NotI-SacI linker (from Fig. 1)

<400> 86
tgataatcta gagcggccgc caccgcggtg gagctc 36